

Fig. 1A

Fig. 1B

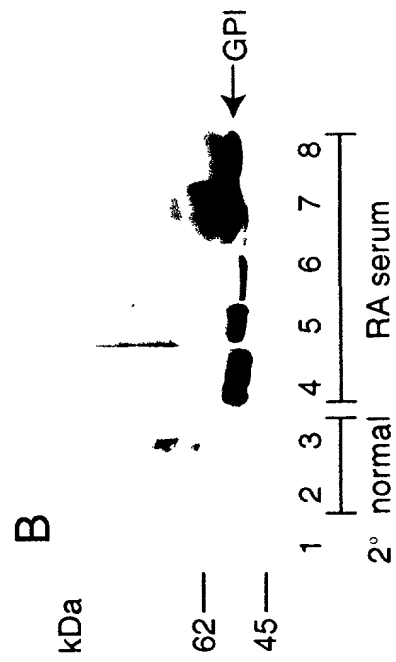


Fig. 1B

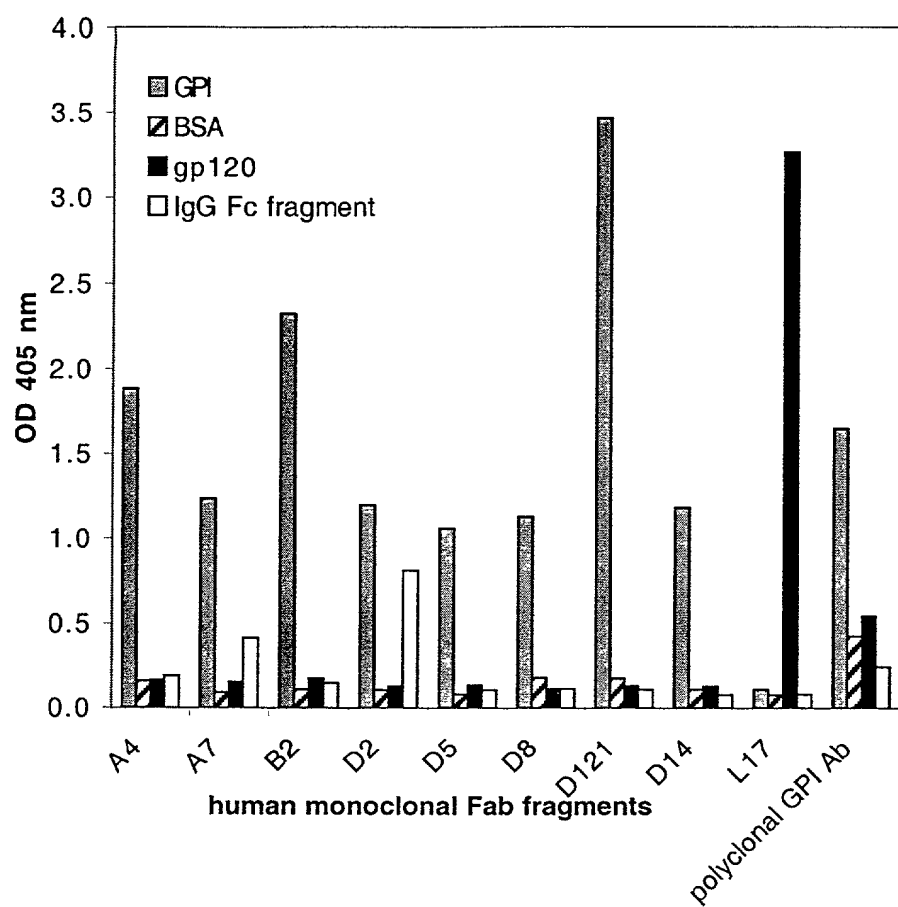


Fig. 2

FIG. 3AL  
**Light Chain Variable AA Sequences**

<u>Name</u>	<u>SEQ ID NO:</u>	FR1	CDR1	FR2
A4	1	PDSLAVSLGERATINC	KSSQSVFYTSNNKNYLA	WYQQKPGQPPKLLIY
D2	2	PSFLSASVGDRVTITC	RASQGISSYLA	WYQLKPGKAPKLLIY
D121	3	PGTSLSPGERATLSC	RASQSVSSSYLA	WYQQKPGQAPRLLIY
B2	4	PDSLAVSLGERATINC	KSSQSVFYTSNNKNYLA	WYQQKPGQPPKLLIY
D14	5	PGTSLSPGEGATLSC	RASQSVSSSYLA	WYQQRPGQAPRLLIY
D5	6	PGTSLSPGEGATLSC	RASQSVSSSYLA	WYQQKPGQAPRLLIY
A7	7	PGTSLSPGERVTLSC	RASQSVSSSYLA	WYQQKPGQAPRLLIY
<u>Name</u> <u>cont'd</u>	CDR2	FR3	CDR3	FR4
A4	WASTRES	GVPDRFSGSGGTDFTLTISSLQAEDVAVYYC	QQYYDSYT	FGQGTKLEIKRTVA
D2	AASTLQS	GVPSRFSGSGGTDFTLTISSLQPEDFATYYC	QQLNSYPLT	FGGGAKEVGIRRTVA
D121	GASSRAT	GIPDRFSGSGGTDFLTISRLEPEDFAVYYC	QQYGSSPRT	FGQGTKVEIKRTVA
B2	WASTRES	GVPDRFSGSGGTDFTLTISSLQAEDVAVYYC	QQYYDSYT	FGQGTKLEIKRTVA
D14	GASSRAT	GIPDRFSGSGGTDFSTISSLQPEDTGTYYC	QQYDNVPDT	FGQGTRELKRTVA
D5	GASSRAT	GIPDRFSGSGGTDFLTISRLEPEDFAVYYC	QQYGTSP	FGQGTRELKRTVA
A7	GASSRAT	GIPDRFSGSGGTDFLTISRLEPEDFAVYYC	QQYGSSPRT	FGQGTKVEIKRTVA

FIG. 3AH  
Heavy Chain Variable AA Sequences

Name	SEQ ID NO.	FR1	CDR1	FR2	CDR2
A4	8	GGGVVQPGRSLKLSCAASGFTFS	SHGSH	WVRQAPGKGLEWVA	LLSSDGSNKFYIESVKG
D2	9	.....AW..LR...V.....	..TM.	.....	..TM.
D121	10	.....R.....	.YTF.	.....	VI.Y..NK.Y.AD....
B2	11	GAEVRKPGTTSVRISCRASGNTFT	GHHIH	WVRQAPGQGLQWMG	RINPTGGGVSLAQSFQD
D14	12	GGGLVQPGGSLRLSCATSGFIFN	SYAMN	WVRQAPGKGLEWVS	RISGNSGSTFYADSVKG
D5	13	GPGLVRPSQTLSLTCPVSPGSIK	GDSYFWS	WVRQPVGKGLEWIG	RIYGRGTTNYNRVFGS
A7	14	GAEVKKPGSSVKVSCRASGGTFS	RYAIS	WVRQAPGQGLEWMG	GIIPFPGFPVNYAQKFQG
Name	cont'd	FR3	CDR3	FR4	VH gene
A4	RFTISKDNSKNTLYLQMNSLRIDDTAVYYCAI		SLVGTTFAPNY	WGQGTILVTVSS	VH3
D2	.....R.....LS...PE.....TN		.E..A...D.	.....	VH3
D121	.....VE.....		.I.....		VH3
B2	RVSLTRDRSSNTVFLELSGLTEEDTALYFCAR		PRFNMIREPLDL	WGQGTVVTVSS	VH1
D14	RFTISRDN SKNTAFLRMNSQRAEDTAVYYCAK		DLSSGAYYYYGMDV	WGQGTTVTVSS	VH3
D5	RVSMVSVDMSRSQFFLELRDVTAA DTAVYYCAR		DKGSEYSYFDP	WGQGI VVNVS	VH4
A7	RVTITADDSTNTAYMGLSSLRSGDTAVYYCAR		VAYDGS GYYNNIPKIYYYSYMD	WGKGTTVTVSS	VH1

V

FIG. 3B

Name	SEQ ID NO:	FR1	CDR1	FR2	CDR2
A4	8	GGGVVQPGRSLKLSCAASGFTFS	SHGSH	WVRQAPGKGLEWVA	LLSSDGSNKFYIESVKG
D2	9	.....AW..LR...V.....	..TM.		..TM.
D121	10	.....R.....	.YTF.		VI.Y..NK.Y.AD.....
DP-46		.....R.....	.YAM.		VI.Y.....AD.....
B2	11	GAEVRKPGTTSVRISCRASGNTFT	GHHIH	WVRQAPGQGLQWMG	RINPTGGGVSLAQSFQD
DP-7		....K...A..KV..K...Y...	SYMH	.....E...	I...S..ST.Y..K..G
D14	12	GGGLVQPGGSLRLSCATSGFIFN	SYAMN	WVRQAPGKGLEWVS	RISGNSGSTFYADSVKG
VH26		.....A...T.S	.....S		A...SG...Y.....
D5	13	GPGLVRPSTLSLTCVPSPGSIK	GDSYFWS	WVRQPVGKGLEWIG	RIYGRGTTNYNRVFGS
IGHCAK		....K.....T..G...S	SG..Y..	.I...A.....	...TS.S....PSLK.
A7	14	GAEVKKPGSSVKVSCRASGGTFS	RYAIS	WVRQAPGQGLEWMG	GIIPPFPGPVNYAQKFQG
VH1-69		.....K.....	S....	.....	....I..TA.....

FIG. 3B CONT'D

Name cont'd	FR3	CDR3	FR4	VH gene
A4	RFTISKDNSKNTLYLQMNSLRIDDTAVYYCAI	SLVGTTFNFY	WGQGTLLVTVSS	VH3
D2	....R.....LS...PE.....TN	.E..A...D.	.....	VH3
D121	.....VE.....	.I.....		VH3
DP-46	....R.....AE.....R			
B2	RVSLTRDRSSNTVFLELSGLTEEDTALYFCAR	PRFNMIREPLDL	WGQGTVVTVSS	VH1
DP-7	..TM...T.TS..YM...S.RS...V.Y...			
D14	RFTISRDNKNTAFLRMNSQRAEDTAVYYCAK	DLSSGAYYYYGM	WGQGTTVTVSS	VH3
VH26	.....LY.Q...L.....	DV		
D5	RVSMVSVDMSRSQFFLELRDVTAAADTAVYYCAR	DKGSEYSYFDP	WGQGIVVNVFS	VH4
IGHCAK	..TI...T.KN..S.K.SS.....			
A7	RVTITADDSTNTAYMGLSSLRSRSGDTAVYYCAR	VAYDGSYYNNI	WGKGTTVTVSS	VH1
VH1-69	.....K..S....E.....E.....	PKIYYYSYMDV		

FIG. 3C

Clone	Closest Germline	% amino acid homology	% nucleotide homology	R/S ratio FRs	R/S ratio CDRs
A4	DP-46	86	89	6/6:1.0	12/5:2.4
D2	DP-46	87	92	8/6:1.3	4/5:0.8
D121	DP-46	91	95	2/4:0.5	7/0:>7.0
B2	DP-7	67	79	20/17:1.2	14/5:2.8
D14	VH26	87	93	7/3:2.3	5/2:2.5
D5	IGHCAK	73	81	17/16:1.1	13/4:3.3
A7	VH1-69	90	94	7/2:3.5	5/0:>5.0



FIG. 4A  
**CDR's Heavy Chain**

SEQ ID NO:	CDR1	SEQ ID NO:	CDR2	SEQ ID NO:	CDR3
15	SHGSH	22	LLSSDGSNKFYIESVKG	29	SLVGTTFANY
16	. .TM.	23	.IFY.....Y.AD....	30	.E..A...D.
17	.YTF.	24	VI.Y..NK.Y.AD....	31	.I.....
18	GHHIH	25	RINPTGGGVSLAQSFQD	32	PRFNMIREPLDL
19	SYAMN	26	RISGNSGSTFYADSVKG	33	DLSSGAYYYYGMDV
20	GDSYFWS	27	RIYGRGTTNYNRVFGS	34	DKGSEYSYFDP
21	RYAIS	28	GIIPFPGPVNYAQKFQG	35	VAYDGSGYNNIPKIYYYSYMDV

**CDR's Light Chain**

SEQ ID NO:	CDR1	SEQ ID NO:	CDR2	SEQ ID NO:	CDR3
36	KSSQSVFYTSNNKNYLA	43	WASTRES	50	QQYYDSYT
37	RASQGISSYLA	44	AASTLQS	51	QQLNSYPLT
38	RASQSVSSSYLA	45	GASSRAT	52	QQYGSSPRT
39	KSSQSVFYTSNNKNYLA	46	WASTRES	53	QQYYDSYT
40	RASQSVSSSYLA	47	GASSRAT	54	QQYDNPDPDT
41	RASQSVSSSYLA	48	GASSRAT	55	QQYGTSPPL
42	RASQSVSSSYLA	49	GASSRAT	56	QQYGSSPRT

FIG. 4B  
**Framework Regions, Heavy Chain**

SEQ ID	FR1	SEQ ID	FR2
NO:		NO:	
57	GGGVVQPGRSLKLSAASGFTFS	64	WVRQAPGKGLEWVA
58	.....AW..LR...V.....	64	.....
59	.....R.....	64	.....
60	GAEVKPGTSVRISCRASGNTFT	65	WVRQAPGQGLQWMG
61	GGGLVQPGGSLRLSCATSGFIFN	66	WVRQAPGKGLEWVS
62	GPGIVRPSQTLTLTCPVSPGSIK	67	WVRQPVGKGLEWIG
63	GAEVKKPGSSVKVSCRASGGTFS	68	WVRQAPGQGLEWMG
SEQ ID	FR3	SEQ ID	FR4
NO:		NO:	
69	RFTISKDNSKNTLYLQMNSLRIDDTAVYYCAI	76	WGQGTLLVTVSS
70	.....R.....LS...PE.....TN	76	.....
71	.....VE.....	76	.....
72	RVSLTRDRSSNTVFLELSGLTEEDTALYFCAR	77	WGQGTIVTVSS
73	RFTISRDN SKNTAF LRMNSQRAEDTAVYYCAK	78	WGQGTIVTVSS
74	RVSMVDMRSRQFFLELRDVTAA DTAVYYCAR	79	WGQGI VVN VFS
75	RV TITADDSTNTAYMGLSSLRS GDTAVYYCAR	80	WGKGTTVTVSS

FIG. 4B cont'd  
**Framework Regions, Light Chain**

SEQ ID NO:	FR1	SEQ ID NO:	FR2
81	PDSLAVSLGERATNC	88	WYQQKPGQPPKLLIY
82	PSFLSASVGDRTTTC	89	WYQLKPGKAPKLLIY
83	PGTSLSPGERATLSC	90	WYQQKPGQAPRLLIY
84	PDSLAVSLGERATNC	91	WYQQKPGQPPKLLIY
85	PGTSLSPGEGATLSC	92	WYQQRPGQAPRLLIY
86	PGTSLSPGEGATLSC	93	WYQQKPGQAPRLLIY
87	PGTSLSPGERVTLSC	94	WYQQKPGQAPRLLIY
SEQ ID NO:	FR3	SEQ ID NO:	FR4
95	GVPDRFSGSGTDFLTISLQAEDVAVYYC	102	FGQGTKLEIKRTVA
96	GVPSRFSGSGTEFTLTISLQPEDFATYYC	103	FGGGAKEVGIRRTVA
97	GIPDRFSGSGTDFLTISRLEPEDFAVYYC	104	FGQGTKVEIKRTVA
98	GVPDRFSGSGTDFLTISLQAEDVAVYYC	105	FGQGTKLEIKRTVA
99	GIPDRFSGSGTDFSTISLQPEDTGTYC	106	FGQGTRLEIKRTVA
100	GIPDRFSGSGTDFLTISRLEPEDFAVYYC	107	FGQGTRLEIKRTVA
101	GIPDRFSGSGTDFLTISRLEPEDFAVYYC	108	FGQGTKVEIKRTVA

FIG. 5A

LIGHT CHAIN NUCLEOTIDE SEQUENCE OF ANTI-GPI ANTIBODIES

A4 – SEQ ID NO:112

CCAGACTCCCTGGCTGTCTCTGGCGGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTTACACTTCCAAACAATAA  
GAACTACTTAGCTTGTAACAGCAGAAACCAGCCAGCCTCCTAAGTTGCTCATTTACTGGGCATCCACCCGGGAATCCGGGGTCC  
CTGACCCGATTTCAGTGGCAGCGGGTCTTGGGACAGATTTCACCTCACCATCAGCAGCCTGCAGGTGAAGATGTGGCAGTTTATTAC  
TGTGAGCAATATTATGATTCTGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAACGAACTGTGGCT

D2 – SEQ ID NO:113

CCATCCTTCCTGTCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCCAGTCAAGGCATTAGCAGTTATTAGCCTGGTAT  
CAGCTAAACCGGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCACTTGCATAAGTGGGTCCCATCAAGGTTACGGGCAG  
TGGATCTGGGACAGAAATTCACCTCTCAATAAGCAGCCTGCAGCCTGAAAGATTTIGCAACTTATTACTGTCAACAGCTTAATAGTT  
ACCTCTCACTTTCGGCGGAGGGGCCAAGGTGGGATCAGACGAACTGTGGCT

D121 – SEQ ID NO:114

CCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCTCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTTAGCCTG  
GTACCAAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGGTGCAATCAGCAGGGCCACTGGCATCCAGACAGGTTCACTG  
GCAGTGGGTCTGGGACAGACTTCACCTCTCACCATCAGCAGACTGGAGCCTGAAAGATTTTGCAGTGTATTACTGTACGAGTATGGT  
AG CTCACCTCGGACGTTCCGCCAAGGGACCAAGGTGGAAATCAAAACGAACTGTGGCT

B2 – SEQ ID NO:115

CCAGACTCCCTGGCTGTCTCTGGCGGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTTACACTTCCAAACAATAA  
GAACTACTTAGCTTGTAACAGCAGAAACCAGCCAGCCTCCTAAGTTGCTCATTTACTGGGCATCCACCCGGGAATCCGGGGTCC  
CTGACCCGATTTCAGTGGCAGCGGGTCTTGGGACAGATTTCACCTCACCATCAGCAGCCTGCAGGTGAAGATGTGGCAGTTTATTAC  
TGTGAGCAATATTATGATTCTGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGAACTGTGGCT

FIG. 5A cont'd

D14 – SEQ ID NO:116

CCAGGCACCCCTGTCAATTGTCTCCAGGGGAAGGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACCTAGCCTG  
GTATCAGCAGAGACCTGGCCAGGCTCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACCCGGCATCCCAGACAGATTTCAGTG  
GAAGTGGATCTGGGACAGATTTCAGTTTCACCATCAGCAGTCTGCAGCCTGAAGATACTGGGACATATTACTGTCAACAATATGAT  
AATGTCCCTGACACTTTTGGCCAGGGGACCAAGGCTGGAGATCAACCGAACTGTGGCT

D5 – SEQ ID NO:117

CCAGGCACCCCTGTCTTTGTCTCCAGGGGAAGGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTG  
GTACCCAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGGTGCATCCAGTAGGGCCACTGGCATCCCAGACAGGTTTCAGTG  
GCAGTGGGTCTGGGACAGACTTCACCTCACCATCAGCAGACTGGAGCCTGAAGATTTCAGTGTATTACTGTACGACGTATGGT  
ACCTCACCCCTCTTCGGCCAAAGGACACGACTGGAGATTAAACGAACTGTGGCT

A7 – SEQ ID NO:118

CCAGGCACCCCTGTCTTTGTCTCCAGGGGAAGAGTCACCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGTTACTTAGCCTG  
GTACCCAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTTCAGTG  
GCAGTGGGTCTGGGACAGACTTCACCTCACCATCAGCAGACTGGAGCCTGAAGACTTTTGCAGTTTACTGTACGACGTATGGA  
AGCTCACCTCGGACGTTCTGGCCAAAGGACCAAGGTGGAAATCAACGAACTGTGGCT

FIG. 5B

HEAVY CHAIN NUCLEOTIDE SEQUENCE OF ANTI-GPI ANTIBODIES

A4-H – SEQ ID NO:116

GAGGCGTGGTCCAGCCTGGAGGTCCCTGAAACTCTCCTGTGCAGCCTCTGGATTACATTCAGTAGTCATGGCTCGCACTGGGTC  
CGCCAAAGCTCCAGGCAAGGGCTGGAGTGGGTGGCACTTTGTGCTGTGATGGAAGTAATAATTCTATATAGAAATCCGTGAAGG  
GCCGATTCACCATCTCCAAGGACAATTCTAAGAACACACTGTATCTGCAAAATGAAACAGCCTGAGAAATTGACGACACGGCTGTCTAT  
TACTGTGCGATTTCCTGGTGGAACTACCGCTTTTAACTACTGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA

D2-H – SEQ ID NO:117

GGCGTGGTCCAAGCATGGAGGTCCCTAAGACTCTCCTGTGTAGCCTGTGGATTACCTTCAGTAGTCATACCATGCACCTGGGTCCG  
CCAGGCTCCAGGCAAGGGCTGGAGTGGGTGGCACTTATATCTATGATGGAAGTAATAATACTATGCAGACTCCGTGAAGGCG  
CGATTCAACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATTGAGCAGCCTAAGACCTGAGGACACGGCTGTCTATTA  
TTGTACGAATTCCGAGGTGGAGCTACCGCTTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCAG

D121-H – SEQ ID NO:118

GGGAGGCGTGGTCCAGCCTGGAGGTCCCTGAGACTTTTCCCTGTGCAGCCTCTGGATTACCTTCAGTTCCCTATACATTCCACTGG  
GTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGGTGGCACTTATATCATATATGATGAAACAAGAAATACTACGCAGACTCCGTGA  
AGGGCCGATTCAACCATCTCCAGAGACAATTCCAAGAACACACTCTATATCTGCAAAATGAACAGCCTGAGAGTTGAGGACACGGCTGTT  
TATTACTGTGCGATTTCCTAGTGGGAACCTACCGCTTTTAACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTC

B2-H – SEQ ID NO:119

GGGGCTGAGGGTGAAGAGCCCGGACCTCCGTGAGGATCTCTTGCAAGGGCATCTGGAAAACACCTTCACTGGCCACCATATTCACCTG  
GGTCCGCCAGGCCCTGGACAAAGCCCTTCAGTGGATGGGAAGAAATCAACCCGACTGGCGGGCGGTAGTCTCGCACAGAGTTTC  
CAGGACAGAGTCAGCCTGACCCAGGACAGGTCTCCAAATACAGTCTTCTTGAACTGAGCGGCTTCACGGAGGAGGACACGGCCT  
TATAATTCTGTGCGAGGCCCGGATTTAACAATGATCCGGGAACCTCTTGACCTCTGGGGCCAGGGGACAGTGGTCAACCGTCTCCTCA

D14-H – SEQ ID NO:120

GGGGGAGGCTTGTAACAGCCCTGGGGGTCCCTGAGACTCTCCTGTGCAACCTCTGGATTCATCTTTAAACAGCTATGCCATGAACTG  
GGTCCGCCAGGCTCCAGGGAAGGGCTTGAGTGGTCTCACGTATTAGTGGAATAGTGGAAGCACATTTCTACGCAGACTCCGTG  
AAGGCCGGTTCACCATCTCCAGAGACAAATTCCAAGAACACACGGCGTTCTGCGAATGAACAGCCAGAGAGCCGAAGACACGGCGG  
TTTATTACTGTGCGAAAGATCTGTGCGAGTGGTGTCATACTACTACGGGATGGACGTCTGGGGCCAGGGGACACCGTCAACCGTC  
TCCTCA

D5-H – SEQ ID NO:121

GGCCCAGGATTGGTGAGGCCATCACAGACCCTATCCCTCACCTGCACCTGTCTCTCCAGGCTCCATTAAAGGTGATAGTTACTTCTGG  
AGCTGGGTCCGTACGCCGTAGGGAAGGACTGGAGTGGATAGGGCGTATCTACGGCAGAGGGACTACCAATTACACCCGTGTT  
TCGGGAGTCGAGTCAGTATGTCAGTGGACATGTCCAGGAGTCAGTTTTTCTTGGAATTGAGAGATGTGACCGCCGACACGGCC  
GTCTATTACTGTGCGAGAGACAAGGGGTCCGAATACTCCTACTTTGACCCCTGGGGCCAGGGGAATAGTGGTCAACGTCTTCTCA

FIG. 5B CONT'D

A7-H – SEQ ID NO:122

GGGCTGAGGTGAAGAACCTGGGTCCCTCGGTGAAGGTCTCCTGCAGGGCTTCTGGAGGCACATTCAGCAGATATGCTA  
TCAGCTGGGTGCGACAGGCCCTGGACAAAGGCTTGAGTGGATGGGAGGGATCATCCCTCCCTTTGGTCCAGTAAACT  
ACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGATTCCACGAAACACAGCCTACATGGGTCTGAGCAGCC  
TGAGATCTGGGGACACGGCCGTGTATTACTGCGCGAGAGTGGCCTATGATGGTAGTGGCTATTACAACAATATCCCAA  
AGATCTACTACTCTCTACATGGACGTCTGGGGCAAGGGACCACGGTCACCCGTGTCTCTCAGC



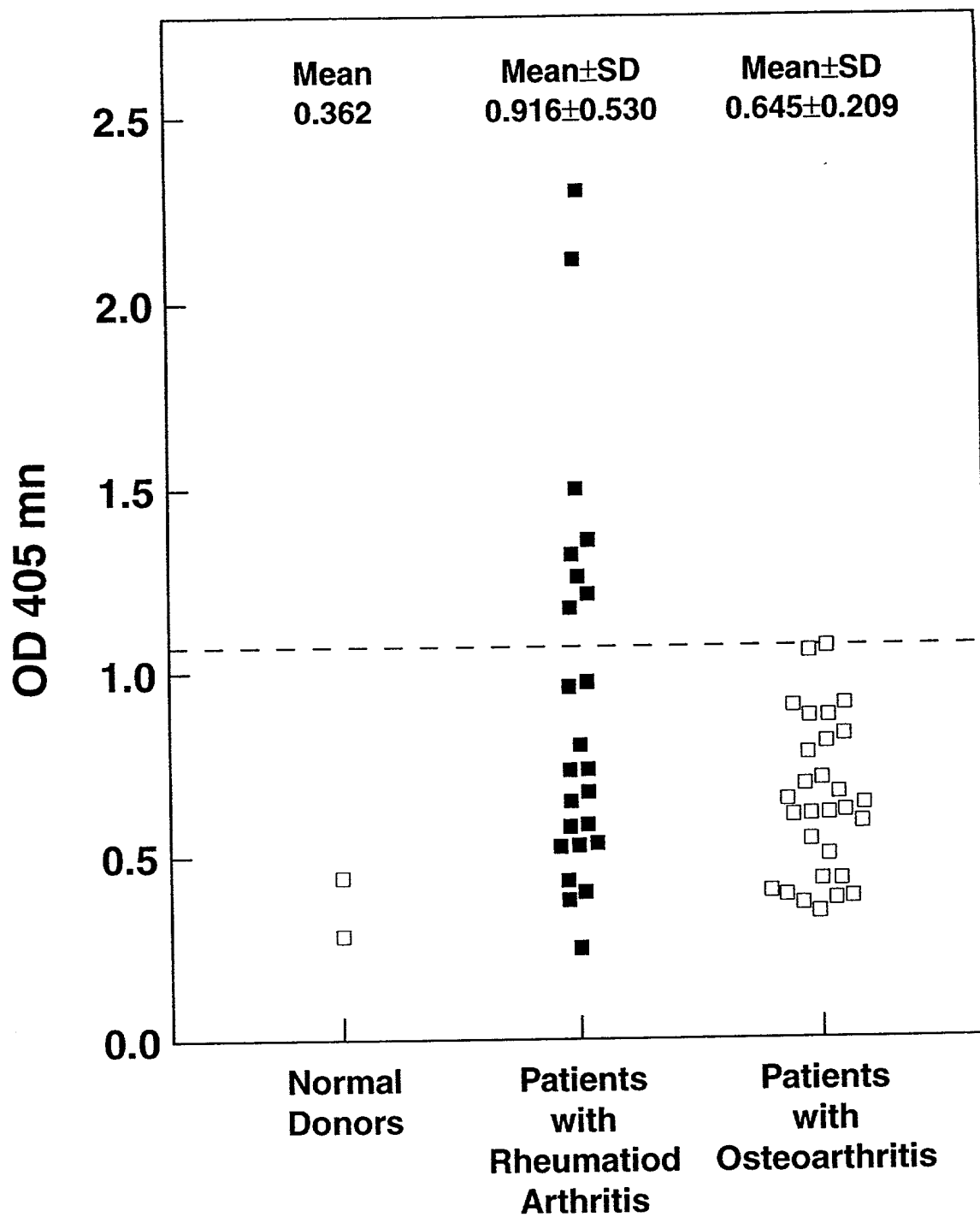


Fig. 6

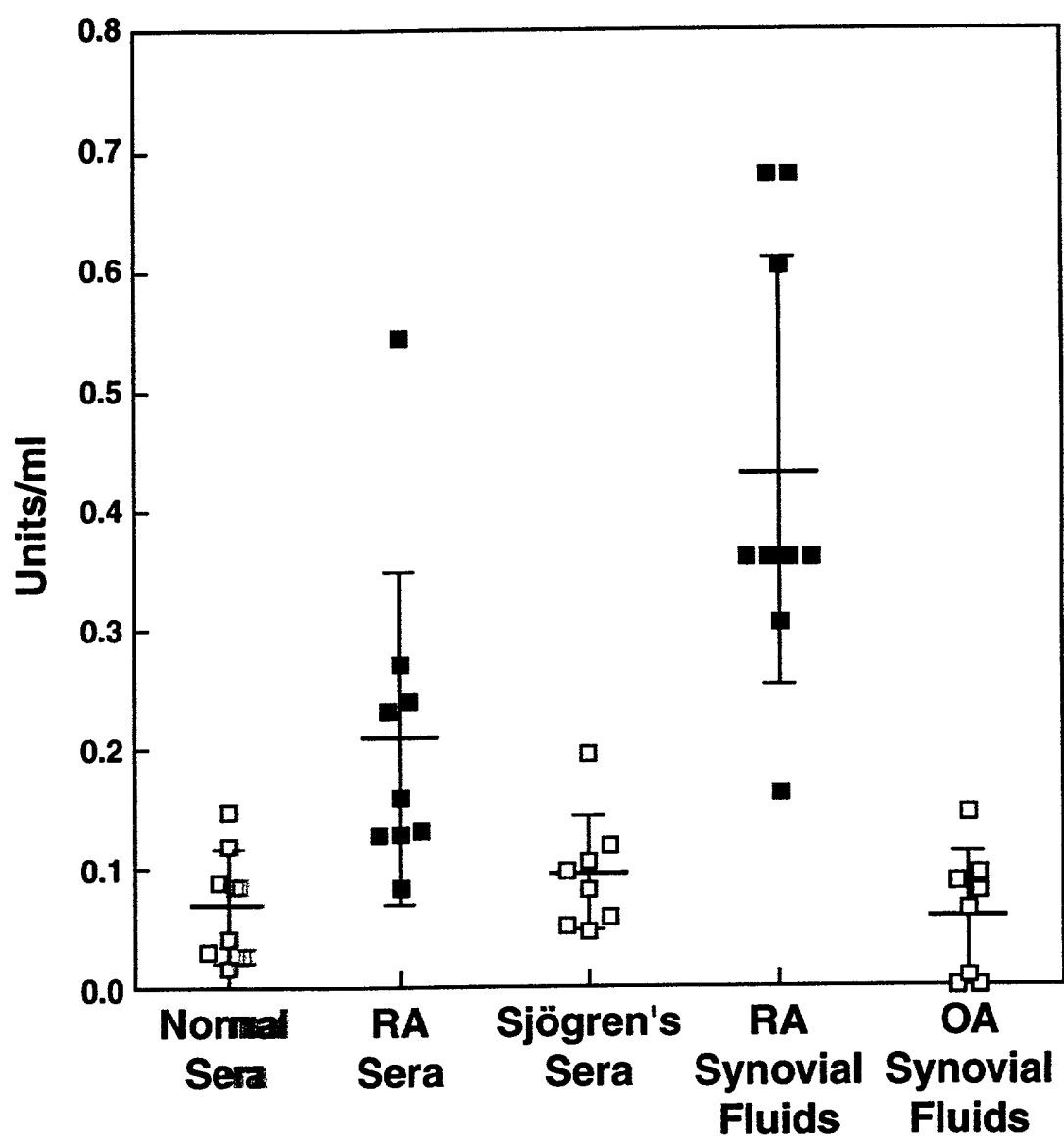


Fig. 7



Fig 9

